THE INFLUENCE OF THE COMPOSITION OF FOOD MATERIALS ON THE GUT FLORA OF EISENIA LUCENS (WAGA 1857)

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ВЛИЯНИЕ СОСТАВА ПИЩИ НА МИКРОФЛОРУ КИШЕЧНИКА У ДОЖДЕВОГО ЧЕРВЯ EISENIA LUCENS (WAGA, 1857)

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Eisenia lucens (Waga 1857) is an earthworm species of particular ecological behaviour. Under natural circumstances it burrows mostly in decaying stumps (frequently in those of the beech: Fagus silvatica) consuming the decomposing wood materials rich in cellulose and lignins. Under laboratory conditions, however, it is easily reared on a mixture of sawdust and farmyard manure.

As it was shown by many workers(/6/, etc.) actinomycetes are capable of rapid growth in the digestive canal of earthworms and constitute an import-

The total number and composition of microflora in the hind gut contents of Eisenia lucens specimens collected from: natural habitats (A); a laboratory reared population fed by a mixture of sawdust-farmyard manure (B)

Parameters	A	B
Average total number of platable microbes on nutrient agar	$6 \cdot 10^7$ /g wet fecal matter	$8.3 \cdot 10^5$/g wet fecal matter
Total actinomycete counts on glycerol arginine agar	$16 \cdot 10^5$ /g wet fecal matter	$2.9 \cdot 10^5$ /g wet fecal matter
Average percentage of actinomycetes in total platable microflora	10%	50%
Number of investigated actinomycete isolates	145	254
Dominant *Streptomyces* species (percentage among all isolates)	*Streptomyces lipmanii* (84.0%)	*Streptomyces olivaceus* (70.9%) *Streptomyces levoris* (11.0%)
Other bacteria	*Pseudomonas fluorescens* (38.3%) *Vibrio* sp. (34.4%)	*Pseudomonas* sp.(present) *Vibrio sp.*(present)

ant co-dominant fraction in the indigenous gut microbiota of these animals. Unfortunately, little is known about the composition at generic or species level of these complex intestinal actinomycete populations, as well as their activities and the role in the gut metabolism.

Numbers and composition of microflora in the gut of Eisenia luceus are shown in the Table.

The aerobic and facultatively anaerobic hindgut-flora of *Eisenia lucens* specimens collected from decaying beech stumps was characterized by the simultaneous coexistence of large populations of a *Vibrio* sp., *Pseudomonas fluorescens* /2,3/ and *Streptomyces lipmanii* /1/. This particular composition of the gut flora detected by us clearly showed that in the earthworms intestinal milieu the natural selection eliminates many external microorganism species and let multiply only a few ones possessing fitness traits.

It was questionable, however, whether this specific community structure of the gut microflora can remain stable or not under the influence of changing food composition and feeding habitats. In the framework of a second experimental series on cultivating of these animals on a mixture of sawdust and farmyard manure under laboratory conditions definite changes in the gut flora were detected. In this case another *Streptomyces* species, *S.olivaceus* proved

to be a common gut colonizer, forming about 70% of the gut actinomycete fraction. This streptomycete, a widely distributed soil microorganism,occurs otherwise in the gut of several earthworms (Lumbricus polyphemus, Fitzingeria platyura depressa, Allolobophora rosea, etc.) /4,5/ more frequently than many other Streptomyces species. A second less frequent but typical Streptomyces species was also found in the gut contents of E.lucens specimens reared under laboratory conditions: S.levoris. This latter belongs to the large variable Griesus-group of streptomycetes within which it shows the closest similarity to S.lipmanii. S.lipmanii and S.levoris differ only in the utilization of a few diagnostic carbon compounds /7/ and they are, presumedly, synonymous species, possessing identical ecological behaviour. Accordingly the gut actinomycete fraction of E.lucens involves both changing and stable elements. Vibrio- and Pseudomonas-isolates were also obtained from the gut contents of laboratory reared E.lucens specimens. This finding renders probable that perhaps these genera are also stable or at least frequently occurring members of the gut flora.

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